



SEQ ID NO: 5
SEQ ID NO: 6
SEQ ID NO: 7
SEQ ID NO: 8
SEQ ID NO: 9
SEQ ID NO: 10
SEQ ID NO: 11
SEQ ID NO: 12
SEQ ID NO: 13
SEQ ID NO: 14

Sequences (3:10) Aligned. Score: 10
Sequences (4:5) Aligned. Score: 42
Sequences (4:6) Aligned. Score: 42
Sequences (4:7) Aligned. Score: 42
Sequences (4:8) Aligned. Score: 42
Sequences (4:9) Aligned. Score: 43
Sequences (4:10) Aligned. Score: 42
Sequences (5:6) Aligned. Score: 92
Sequences (5:7) Aligned. Score: 63
Sequences (5:8) Aligned. Score: 62
Sequences (5:9) Aligned. Score: 64
Sequences (5:10) Aligned. Score: 63
Sequences (6:7) Aligned. Score: 63
Sequences (6:8) Aligned. Score: 62
Sequences (6:9) Aligned. Score: 63
Sequences (6:10) Aligned. Score: 61
Sequences (7:8) Aligned. Score: 98
Sequences (7:9) Aligned. Score: 97
Sequences (7:10) Aligned. Score: 91
Sequences (8:9) Aligned. Score: 96
Sequences (8:10) Aligned. Score: 93
Sequences (9:10) Aligned. Score: 90

```

mSorLA      YA QYLWITFDFCST INHFSIPFRAAD LLLHSKASNLLLGDRSHPNKQLW KSDDFGQTWI 60
mSort       -----
Vps10p      -----MILLH 65

```

mSorLA MI QEHVKSFSWGID PYDQPNAIYIER HEPFGFSTVLRSTDFQSRNQEVILEEVRDFQL 120
mSort -----
Vps10p FV YSLWALLLIPLI NAEFTPKVTKT IAQDSFEILSFDDSNLIRKODAS VTISFDDGET 65

```

mSorLA      RD KYMFATKVHLP GSQQQSSVLWV SFGKPMRAAQFVTKHPINEYYIA DAAEDQVFVC 180
mSort       -----MERPRG AADG----- 10
Vps10p      WE KVEGIEDEITWI YIDPFNRHRAVATSMYESRLYITNDQGSWERITLPDSEK---NI 122
mCS2        -----MA HRGPPSAPKRPG PTAPDRSFQA 24
hCS3        -N MEAAARTERPAGR PGAPLVRTGLLLLSTWVLAGEIT WDATGGPGRAAPASRPPALSP 59
mCS3        -- MEAAAGTERPAGWPGAPLARTGLLLLSTWVLAGEIT WGATGGPGRLVS PASRPPVLPP 58
mCS1a       MG KVGAGDGY SAG- LSALLAGAGLML-----LAPGVCSLSLSCPPQHPSSTPR----RT 50
mCS1b       MG KVGAGDGSSAG- LSALLAGAGLML-----LAPGVCSLSLSCPPQHPSSTPR----RT 50
mCS1c       MG KVGAGDGS SAG- LSALLAGAGLML-----LAPGVCSLSLSCPPQHPSSTPR----RT 50
hCS1        MG KVGAGGGSQAR- LSALLAGAGLLIL-----CAPGVCGGSGCCPSPHPSAPR----SA 50

```

```

mSorLa      VSHSNNSTNLYISE AEGKFSLSLLEN VLYYSPGGAGSD TLVRYFANEFPADFHRVEGLQG 240
mSort       -----LLRWPLGLLLLLLQLPPAAV G---QDRLDAPPPAPPLLRWAGP ----- 51
Vps10p      SS RGCYIETHPLNK NYFLAKNCYCEK TSDVNEENSGDEEGAPVFINTRCTDKVFASNDG 182
mCS2        LPPCWPRSPWPLLLLLLYLVAAACGM GRSPQPGRQGGP GQITRLPAGRT ----- 74
hCS3        LS PRAVASQWPEELASARRAAVLGRR AGPELLPQQGGG RGGEMQVEAGGTS PAGERRGRG 119

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FIG 2A

File: TYPE 2 DIABETES SUSCEPTIBILITY GENES

Inventor(s): Attie/Stoehr/Schueler/Clee

Application No.:

Docket Number: 960296.99080

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mCS3	LLPRAAENRWPEELASARRAAAPRRRSRLLEPL SQASR---GEIR TEAAGMSPEGAR WVPG 115
mCS1a	LT PRGFPHPGPLGR APATPPPLFMR-----PLFAVAPG DRALFLERAGGS-----R 96
mCS1b	LT PRGFPHPGPLGR APATPPPLFMR-----PLFAVAPG DRALFLERAGGS-----R 96
mCS1c	LT PRGFPHPGPLGR APATPPPLFMR-----PLFAVAPG DRALFLERAGGS-----R 96
hCS1	ST PRGFHQGRPGR APATPLPLVVR-----PLFSVAPG DRALSLEARGT-----G 96
mSorLA	VY IATLINGSMNEENMRSVITFDKGGTWEFLQAPFTGYGEKINCELSQGCSSLHLAQRLS 300
mSort	-----VGVSUWGLR AAAPGGPVPRAG RWRRGAPAEQD CGRLP----- 88
Vps10p	GK SFSEIKSSLE-R NENSAISISDCG FAKTGKSDLESSTSIICLFQNM QLIMDEFSS- 240
mCS2	---ESGDRKDPQAR ESEPSVPGLPGPSASGPSTDGAPAPGKRRRARVPVAGAASASR-- 129
hCS3	IPAPAKLGARRSRRAQPPITQERGD AWATAPADGSR--GSRPLAKGSREEVKAPRAGG- 176
mCS3	IP SPSQAGSARRTRRAQPPSPLERGD SWATALADGAK--GSRPHTKGSREEVRATRTGG- 172
mCS1a	VS VATAARSGRRRR SGTEPEKIEPGE GASRSRRDMLKD GGQQGLGTGARD PGKATRFR-- 154
mCS1b	VS VATAARSGRRRR SGTEPEKIEPGE GASRSRRDMLKD GGQQGLGTGARD PGKATRFR-- 154
mCS1c	VS VATAARSGRRRR SGTEPEKIEPGE GASRSRRDMLKD GGQQGLGTGARD PGKATRFR-- 154
hCS1	AS MAVAARSGRRRR SGADQEKAEERGE GASRSPRGVLRD GGQQEPGTRERD PDKATRFR-- 154
	^furin? ^furin? :
mSorLA	QLNLQLRRMPILS KESAPGLIATGVSUKNLASKTNV YISSSAGARWRE ALPGPHYTYW 360
mSort	-----DFIA KLTNNTHQHVFDLSSGSVSLSW 114
Vps10p	-----PYTES KLVLTWDGKSL KEFDQFKDKV 267
mCS2	-----AQV SLISTSFVLKGD ATHNQAMVHW 154
hCS3	-----SAAEDL RLPSTSFALTGD SAHNQAMVHW 204
mCS3	-----ASTEEL RLPSTSFALTGD SAHNQAMVHW 200
mCS1a	-----MEEL RLTSTTFALTGD SAHNQAMVHW 180
mCS1b	-----MEEL RLTSTTFALTGD SAHNQAMVHW 180
mCS1c	-----MEEL RLTSTTFALTGD SAHNQAMVHW 180
hCS1	-----MEEL RLTSTTFALTGD SAHNQAMVHW 180
. : : : :	
mSorLA	GD HGGIIMAIQGM ETNELKYSTNEG ETWKTFFVSEKPVFVYGLLTPGE KSTVFTIFGS 420
mSort	VG DSTGVILVLTTF QVPLVIVSFGQS KLYRSEDYGNK----FKDITNLINNTFIRTEFGM 170
Vps10p	VNGYRILKSHMVVI TQGDYNDMSSM DVWVSNDLSNFK MAYMPTQLRHSM QGEIYEDAMG 327
mCS2	TG ENSSVILILTKYH-ADMGKVLLESSLWRSSDFGTT----YTKLTLPQ VTTVIDNF-- 207
hCS3	SGHNSSVILILTKL YD-FNLGSVTESSLWRSTDYGT----YEKLNDKVG LKTIVLSYL-- 257
mCS3	SGHNSSVILILTKL YD-FNLGSVTESSLWRSTDYGT----YEKLNDKVG LKTIVLSYL-- 253
mCS1a	SGHNSSVILILTKL YD-YNLGSITESLWRSTDYGT----YEKLNDKVG LKTIVLSYL-- 233
mCS1b	SGHNSSVILILTKL YD-YNLGSITESLWRSTDYGT----YEKLNDKVG LKTIVLSYL-- 233
mCS1c	SGHNSSVILILTKL YD-YNLGSITESLWRSTDYGT----YEKLNDKVG LKTIVLSYL-- 233
hCS1	SGHNSSVILILTKL YD-YNLGSITESLWRSTDYGT----YEKLNDKVG LKTIVLSYL-- 233
. : : : :	
mSorLA	NK ESVHSLILQVN ATDALGVPCTEN DYKLWSPSDERGNECLLGHKTVFKRRTPHATCFN 480
mSort	-----AIGPENSGKVILTAEVSG ----- 188
Vps10p	-----RIILPMS RERSDQED----- 343
mCS2	-----YICPAN KRKIILVSSSL----- 224
hCS3	-----YVNPTN KRKIMLLSD----- 272
mCS3	-----YVNPTN KRKIMLLSD----- 268
mCS1a	-----YVCPTN KCKIMLLTD----- 248
mCS1b	-----YVCPTN KCKIMLLTD----- 248
mCS1c	-----YVCPTN KCKIMLLTD----- 248
hCS1	-----YVCPTN KRKIMLLTD----- 248
. : : : :	
mSorLA	GEDFDRPVVVSNCSTREDYECDFGF KMSEDLSLEVCVPDPEFFGKPYSPVPVPGVSSY 540
mSort	GS RGGRVFRSSDFA KNFVQTDLPFHP-----LTQMMYS PQNSDYLLALST ENGLWVSKNF 243
Vps10p	KG IVSEILISDSQG LKFSPIPTANE VFG-YINLYQPTYLKGTMIASLYPLSRRNRKKG 402
mCS2	GD REQSLFLSTDEG ATFQKYPVPFL-----VETLLFH PKEEDKVLAYTK DSKLYVSSDL 278

FIG 2B

Title: TYPE 2 DIABETES SUSCEPTIBILITY GENES

Inventor(s): Attie/Stoeck/Schueler/Clee

Application No.:

Docket Number: 960296.99080

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hCS3	PEMESSILISSDEGATYQKY RLTFY-----I QSLLFH PKQEDWVLAYS LDQKLYSSMDF 326
mCS3	PE MESSVLISSDEGATYQKYRLTFY-----IQSLLFH PKQEDWVLAYS LDQKLYSSMDF 322
mCS1a	PE IESSLLISSDEGATYQKYRLNFI-----LQSLLFH PKQEDWILAYSQ DQKLYSSAEF 302
mCS1b	PE IESSLLISSDEGATYQKYRLNFI-----LQSLLFH PKQEDWILAYSQ DQKLYSSAEF 302
mCS1c	PE IESSLLISSDEGATYQKYRLNFI-----LQSLLFH PKQEDWILAYSQ DQKLYSSAEF 302
hCS1	PE IESSLLISSDEGATYQKYRLNFI-----IQSLLFH PKQEDWILAYSQ DQKLYSSAEF 302

mSorLA	RR TRGYRKISGDTCSGGDVEARLEGE LVPCLAEENEFILYAMRKFIYRY DLASGATEQL 600
mSort	G--EKWEEIHK-----AVCLAK WGPNNIIFFTH VNGSCKADLGAL ELWRTSDLGK 292
Vps10p	AK GVKNGKGVTKISV DNGLTWTVLKVV DPNADSFDCDI TDFENC SLQNMFI YTGREGSTPTA 462
mCS2	G--KKWTLQERVT KDHVFWAVSGVDDPNLVHVEAQD LSGGYRYTCL IYNC SAQPHIA 336
hCS3	G--RRWQLMHERIT PNRFYWSVAGLD KEADLVHMEVRTTDGYAHYLT CRI QECAETTRSG 384
mCS3	G--RRWQLMHERIT PNRFYWSVAGLD KEADLVHMEVRT ADGYAHYLT CRI QECAETTRSG 380
mCS1a	G--RRWQLIQESVVPNRFYWSVMGSS KEPDLVHLEART VDGHSIYLT CRM QNCTEANRNK 360
mCS1b	G--RRWQLIQESVVPNRFYWSVMGSS KEPDLVHLEART VDGHSIYLT CRM QNCTEANRNK 360
mCS1c	G--RRWQLIQESVVPNRFYWSVMGSS KEPDLVHLEART VDGHSIYLT CRM QNCTEANRNK 360
hCS1	G--RRWQLIQEGVVPNRFYWSVMGSSN KEPDLVHLEART VDGHSYLT CRM QNCTEANRNQ 360

mSorLA	PL SGLRAAVALDFGYERNCLYWSDLALDTIQRCLNGSTGQEVII NSGLE TVEALAFEPL 660
mSort	TF KTIG-----VKIYSFG LGGRFLFASE 315
Vps10p	GILMTTG-----IV GDGSVFDWGDQR TFI SRDGGTLWK LAFDFPCLYAVG DYGNVIVAIP 517
mCS2	PF SGP-----IDRGS LT VQDEYIFLKA 358
hCS3	PFARS-----IDISSLVVQDEYIFIQV 406
mCS3	PFARS-----IDISSLVVQDEYIFIQV 402
mCS1a	PFPGY-----IDPDSLIVQDDYVVFVQL 382
mCS1b	PFPGY-----IDPDSLIVQDDYVVFVQL 382
mCS1c	PFPGY-----IDPDSLIVQDDYVVFVQL 382
hCS1	PFPGY-----IDPDSLIVQDDYVVFVQL 382

mSorLA	SQ LLYWVDAGFKKI EVANPDGDFRLT IVNSSVLDPRALVLPQEGVMFW TDWGD LKPGI 720
mSort	MA DK---DTTRRIH VSTDQGD TWSMA QLPSVGQE QFYS ILAANEDMVFMH VDE----- 365
Vps10p	YN ADEDDDPQSEFYYS LDQKGTWTEYQLETTIYPNEVM NTTPDGSGAKFILNG-----F 571
mCS2	TS -----TNRTKYVVS YRRSDFVLM KLPKYALPKDMH IISTDEQQVFVAVQE----- 405
hCS3	TT -----SGRASYVVS YRREAF AQI KLPKYSLPKDMH IISTDENQVFVAVQE----- 453
mCS3	TI -----GGRASYVVS YRREAF AQI KLPKYSLPKDMH IISTDENQVFVAVQE----- 449
mCS1a	TS -----GGRPHYVVS YRRSPFAQM KLPKYALPKDMH VISTDENQVFVAVQE----- 429
mCS1b	TS -----GGRPHYVVS YRRSPFAQM KLPKYALPKDMH VISTDENQVFVAVQE----- 429
mCS1c	TS -----GGRPHYVVS YRRSPFAQM KLPKYALPKDMH VISTDENQVFVAVQE----- 429
hCS1	TS -----GGRPHYVVS YRRNFAQM KLPKYALPKDMH VISTDENQVFVAVQE----- 429

mSorLA	YR SYMDGSAAYRLV SEDVKWPNGISV DS-----QWIYWT DAYLDC IERITFSGQQ 770
mSort	---PGDTGFGTIFTSDDRGIVYSKSL DR-----HLYTTTG---E TDFTNVTS LR 409
Vps10p	TLAHMDGTTNFIYAIDFSTAFNDKTC EENDFEDWNLAEGKCVNGVKYKIRRRKQDAQCLV 631
mCS2	---WNQVDTYNLYQS DLRGVYSLVL EN-----VRSSRQAEENVVIDILEVRGVK 452
hCS3	---WNQNDTYNLYI SDTRGIYFTLAL EN-----IKSSRGLMGNI IIELYEVAGIK 500
mCS3	---WNQNDTYNLYI SDTRGIYFTLAL EN-----IKSSRGLMGNI IIELYEVAGIK 496
mCS1a	---WNQNDTYNLYI SDTRGVYFTLAL EN-----VRSSRGPEGNMIDLYEVAGIK 476
mCS1b	---WNQNDTYNLYI SDTRGVYFTLAL EN-----VRSSRGPEGNMIDLYEVAGIK 476
mCS1c	---WNQNDTYNLYI SDTRGVYFTLAL EN-----VRSSRGPEGNMIDLYEVAGIK 476
hCS1	---WNQNDTYNLYI SDTRGVYFTLAL EN-----VQSSRGPEGNMIDLYEVAGIK 476

FIG 2C

Accession	Gene	Protein	Length
mSorLA	RSVILDSLPH	YAIIVFKNEIYWDDWSQLSIFRAS KHSRSQVEILASQLTGLMDMKVY K	830
mSort	GV YITSTLSE	NSI QSMITFDQGRW EHLRKP-ENSKC DA-----	448
Vps10p	KK VFEDLQLF	ETAC DKCTEADYECAP EFVRDATGKCV DYN-----	673
mCS2	GVFLAN-QKV	DGKV TTVITYNKG RDW RLLQAPD VDLRGSP-----	491
hCS3	GIFLAN-QKV	DDQV KTYITYNKG RDW RLLQAPD VDLRGSP-----	539
mCS3	GIFLAN-QKV	DDQV KTYITYNKG RDW RLLQAPD VDLRGSP-----	535
mCS1a	GMFLAN-KKID	NQV KTFITYNKG RDW RLLQAPD ADLRG DP-----	515
mCS1b	GMFLAN-KKID	NQV KTFITYNKG RDW RLLQAPD ADLRG DP-----	515
mCS1c	GMFLAN-KKID	NQV KTFITYNKG RDW RLLQAPD ADLRG DP-----	515
hCS1	GMFLAN-KKID	NQV KTFITYNKG RDW RLLQAPD TDLRG DP-----	515
: . : :			
mSorLA	GK NAGSNACV	PQPCSLCLPKANNSK SCRCPEGVASSVLP SGDLMDCDPQGYQRKNNTCV	890
mSort	-----TAKN	KNECSLHIHASYSISQ KLNVPMA PLSEP NAVGIVIAHG-----	490
Vps10p	IVLSDVCDK	TKKT VPKPLQLVKGD KCKKPM TVKSVD ISCEGV PPKG-----	721
mCS2	-----TNCQ	PPDCYLHLHLRWADNP YVSGTVH--TKD TAPGLIMGAG-----	531
hCS3	-----VHCL	LPFCSLHLHLQ LSENP YSSGRIS--SKE TAPGLVVATG-----	579
mCS3	-----VHCL	LPFCSLHLHLQ LSENP YSSGRIS--SKD TAPGLVVATG-----	575
mCS1a	-----VHCL	LPYCSLHLHLK VSENP YTSGIIA--SRD TAPSIIVASG-----	555
mCS1b	-----VHCL	LPYCSLHLHLK VSENP YTSGIIA--SRD TAPSIIVASG-----	555
mCS1c	-----VHCL	LPYCSLHLHLK VSENP YTSGIIA--SRD TAPSIIVASG-----	555
hCS1	-----VHCL	LPYCSLHLHLK VSENP YTSGIIA--SKD TAPSIIVASG-----	555
: . : :			
mSorLA	KEENTCLR	NQYRCSNGNCINSIWCD FDNDCG DMSDER NCPTTVCDADTQ FRCQESGTCI	950
mSort	-----	-----	-----
Vps10p	-----	-----	-----
mCS2	-----	-----	-----
hCS3	-----	-----	-----
mCS3	-----	-----	-----
mCS1a	-----	-----	-----
mCS1b	-----	-----	-----
mCS1c	-----	-----	-----
hCS1	-----	-----	-----
: : :			
mSorLA	PL SYKCDLE	DDCGD NSDESHCEMHQC RSDEFNCSSGMC IRSSWVCDGDND CRDWSDEANC	1010
mSort	-----SVGD	AISVMVPDVYIS D-----DGGYS WAKMLEGPHY	522
Vps10p	-----TNDK	EIVVTENKDFK IQFYQYFDTVTDESLLMINSRGEA YISHDGGQTI	771
mCS2	-----NLGS	QVVEYKEEMYITS-----DCGHT WRQVFEEHH	563
hCS3	-----NIGP	ELSYTDIGVFISS-----DGGNT WRQIFDEEYN	611
mCS3	-----NIGS	ELSYTDIGVFISS-----DGGNT WRQIFDEEYN	607
mCS1a	-----NIGS	ELSDSDISMFVSS-----DAGNT WRQIFEEHHS	587
mCS1b	-----NIGS	ELSDSDISMFVSS-----DAGNT WRQIFEEHHS	587
mCS1c	-----NIGS	ELSDSDISMFVSS-----DAGNT WRQIFEEHHS	587
hCS1	-----NIGS	ELSDTDISMFVSS-----DAGNT WRQIFEEHHS	587
: : :			
mSorLA	TAIYHTCEAS	NFQCHNGHCIPQRWAC DGDADCQDGSDEDPVSCEKKCNF HCPNGT CIPS	1070
mSort	YT ILDSGGI	IVAIE HSNRPINVIKFSTDEGQC-----WQSYVFTQE	563
Vps10p	RR FDSNGET	IIIEVFNPPYNSAYLF GSKGSIFS-----THDRGYSFMTA	816
mCS2	VL YLDHGGV	IAAIAK DTSIPLKILKFS VDEGHT-----WSTHNFST	604

FIG 2D

title: TYPE 2 DIABETES SUSCEPTIBILITY GENES

Inventor(s): Attie/Stoehr/Schueler/Clee

Application No.:

Docket Number: 960296.99080

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hCS3	VWFLDWGGALVAMKHTPLPVRH LWVSFDEGHS-----WDKYGFTSV 652
mCS3	VWFLDWGGALVAMK HTPLPVRHLWVS FDEGHS-----WDKYGFTLL 648
mCS1a	IL YLDQGGVLVAMK HTSLPIRHLWLS FDEGRS-----WSKYSFTSI 628
mCS1b	IL YLDQGGVLVAMK HTSLPIRHLWLS FDEGRS-----WSKYSFTSI 628
mCS1c	IL YLDQGGVLVAMK HTSLPIRHLWLS FDEGRS-----WSKYSFTSI 628
hCS1	VL YLDQGGVLVAMK HTSLPIRHLWLS FDEGRS-----WSKYSFTSI 628
.	
mSorLA	SK HCDGLRDCPDGS DEQHCEFFCTRFMDVCKNRQQCLFHSMVCDGIVQC RDGSDEDAAF 1130
mSort	PI YFTGLASEPGA----- 576
Vps10p	KLPEARQLGMPLDF N----- 831
mCS2	SVFVDGLLSEPGD----- 617
hCS3	PLFVDGALVEAGM----- 665
mCS3	PLFVDGALVEAGV----- 661
mCS1a	PLFVDGVLGEPGE----- 641
mCS1b	PLFVDGVLGEPGE----- 641
mCS1c	PLFVDGVLGEPGE----- 641
hCS1	PLFVDGVLGEPGE----- 641
.	
: : : : :	
mSorLA	AGCSQDPEFHKECDEFGFCQNGVCI SLIWKCDGMDDCGDYSDEANCENP TEAPNCSRYF 1190
mSort	-----RSMNISIW GFTESFITRQWV SYTVDFKDIL 606
Vps10p	-----AKAQDTFIYYGGKNCESILSPECHAVAYLTNDGGE TITEMLDNAI 876
mCS2	-----ETLVMTVF GHIS--FRSDWE LVKVDFRPSF 645
hCS3	-----ETHIMTVF GHFS--LRSEWQ LVKVVDYKSIF 693
mCS3	-----ETHIMTVF GHFS--LRSEWQ LVKVVDYKSIF 689
mCS1a	-----ETLIMTVF GHFS--HRSEWQ LVKVVDYKSIF 669
mCS1b	-----ETLIMTVF GHFS--HRSEWQ LVKVVDYKSIF 669
mCS1c	-----ETLIMTVF GHFS--HRSEWQ LVKVVDYKSIF 669
hCS1	-----ETLIMTVF GHFS--HRSEWQ LVKVVDYKSIF 669
: : : : :	
mSorLA	QF HCENGHCIPNRW KCDRENDGCDWS DEKDCGDSHVLP SPTPGPSTCLPNYFRCSGACV 1250
mSort	ER NCE-----EDDYTTWLAHSTD-----PGDYKDGC 633
Vps10p	HC EFAGSLFKYPSN EDMVMCQVKEKSSQTRSLVSSTDFQDDKNTVFENIIGYLSTGGYI 936
mCS2	PR QCG-----EDDYSSWD LTDL-----QGHDH 668
hCS3	SR HCT-----KEDYQTHW LLN-----QGEPVCV 715
mCS3	SRRCT-----KEDFETWH LLN-----QGEPVCV 711
mCS1a	DRRCA-----EEDYRPWQ LHS-----QGEACI 691
mCS1b	DRRCA-----EEDYRPWQ LHS-----QGEACI 691
mCS1c	DRRCA-----EEDYRPWQ LHS-----QGEACI 691
hCS1	DRRCA-----EEDYRPWQ LHS-----QGEACI 691
.	
: : : : :	
mSorLA	MGTWVCDGYRDCAD GSDEEACPSLANSTAAPTQLGQCDFEFEC HQPKKCI PNWKRC 1310
mSort	LG -----YKEQFLRLR 644
Vps10p	IVAVPHE-----NNELRAYVTID 954
mCS2	MG -----QQRSYRKRK 679
hCS3	MG -----ERKIFKKRK 726
mCS3	MG -----ERKIFKKRK 722
mCS1a	MG -----AKRIYKKRK 702
mCS1b	MG -----AKRIYKKRK 702
mCS1c	MG -----AKRIYKKRK 702
hCS1	MG -----AKRIYKKRK 702

FIG 2E

tle: TYPE 2 DIABETES SUSCEPTIBILITY GENES

Inventor(s): Attie/Stoehr/Schueler/Clee

Application No.:

Docket Number: 960296.99080

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:: .. ..... :

mSorLA  GHQDCQDQDE ANCPHTSTLTCTSRFKCEDGEAC IVLSERCDFGLD CSEDESDEKACSDE 1370
mSort    KSSVCQNGRDYVVA KQPSVPCPSLED FLCDFGYFRPENAS-----ECVE QPELKGHELE 698
Vps10p   GT EFAEAKFPYDED VGKQEAFTILES EKGSIFLHLATN LVPGRDFGNLLK SNSNGTSFVT 1014
mCS2     STSWCVKGRSFTSALTSRVCKCRDSD FLCDYGFERSSSSESTA--NKCSA NFWFNPLSPP 737
hCS3     PG AQCALGRDHSGS VVSEPCVCANWD FECDYGYERHGE SQ-----CVPAFWYNPASPS 779
mCS3     PG AQCALGREYSGS VVSEPCVCADWD FECDYGYERHGE SQ-----CVPAFWYNPASPS 775
mCS1a    SE RRCMQ--KYAGAMESEPCVCTEAD FDCDYGYERHSNGQ-----CLPAFWFNPSSL 753
mCS1b    SE RRCMQ--KYAGAMESEPCVCTEAD FDCDYGYERHSNGQ-----CLPAFWFNPSSL 753
mCS1c    SE RRCMQ--KYAGAMESEPCVCTEAD FDCDYGYERHSNGQ-----CLPAFWFNPSSL 753
hCS1     SE RRCMQG-KYAGAMESEPCVCTEAD FDCDYGYERHSNGQ-----CLPAFWFNPSSL 754

mSorLA    LT VYKVQNLQWTAD FSGDVTLTWTRP KMPSASCYVNV YYRVVGESIWKT LETHSNTKTST 1430
mSort     FC LYGKEEHLTTNGYR-----KIPGDKCQGM N-----PAREVK----- 732
Vps10p    LE HAVNRNTFGYVD FEKIQGLEGIIL TNIVSNSDKVAE NKEDKQLTKIT FNEGSDWN-- 1072
mCS2      ED CVLGQTYTSSLGYR-----KVVSNNVCEGGV DLQQSPVQLQCPLQAPR----- 781
hCS3      KD CSLGQSYLNSTGYR-----RIVSNNCTDGL REKYTAKAQMCPC GKAPR----- 823
mCS3      KD CSLGQSYLNSTGYR-----RIVSNNCTDGL RDKYSAKTQLCPC GKAPR----- 819
mCS1a     KD CSLGQSYLNSAGYR-----KVVSNNCTDGV REQYTAKPQKPC GKAPR----- 797
mCS1b     KD CSLGQSYLNSAGYR-----KVVSNNCTDGV REQYTAKPQKPC GKAPR----- 797
mCS1c     KD CSLGQSYLNSAGYR-----KVVSNNCTDGV REQYTAKPQKPC GKAPR----- 797
hCS1      KD CSLGQSYLNSTGYR-----KVVSNNCTDGV REQYTAKPQKPC GKAPR----- 798

mSorLA    VL KVLKPDTTYQVK VQVHCLNKVHNTNDFVTLRTPEGLPADAPRNQLSLN REEEGVILGH 1490
mSort     -----DLKKKCTSNFL NPTKQN----- 749
Vps10p    -----FLKPPKRDS EGKFFCCKSSSL DECSLHLHGYTE RKDIRDTYSS 1115
mCS2      -----GLQVSIRGEAVAVRPREDVLFVV RQEQGDVLT 814
hCS3      -----GLHVTTTDGRLVAEQGHNATFIILMEEGDLQRT 856
mCS3      -----GLHVTTTDGRLVAEQGHNATFIILMEEGDLQRT 852
mCS1a     -----GLRIVTADGKL TAEQGHNVTLMV QLEEGDVQRT 830
mCS1b     -----GLRIVTADGKL TAEQGHNVTLMV QLEEGDVQRT 830
mCS1c     -----GLRIVTADGKL TAEQGHNVTLMV QLEEGDVQRT 830
hCS1      -----GLRIVTADGKL TAEQGHNVTLMV QLEEGDVQRT 831

mSorLA    WAPPVHTHGLIREY IVEYSRSGSKMWASQRAASNSTEI KNLLLNALYTVR VAAVTSRGIG 1550
mSort     -----SKSNSVPIILAIVGLMLVTVVAG----- 772
Vps10p    GS ALGMMFGVGNVG PNLLPYKECSTFFTTDGGETWAEV KKTTPHQWEYGDHGGILVLPEN 1175
mCS2      KYQVDLGDGFKAMY VNLTLTGEPIRHHYESPGIYRVSV RAENMAGHDEAVLFVQVNSPLQ 874
hCS3      NI QLDFGDGIIVSY ANFSPIEDGIKH VYKSAGIFQVTA YAENNLGSDTAFLFLHVCPVE 916
mCS3      NI QLDFGDGIIVSY ANFSPIEDGIKH VYKSAGIFQVTA YAENNLGSDTAFLFLHVCPVE 912
mCS1a     LI QVDFGDGIIVSY VNLSSMEDGIKH VYQNVGIFRVTV QVDNSLGSDSAVLYLHVTCPLE 890
mCS1b     LI QVDFGDGIIVSY VNLSSMEDGIKH VYQNVGIFRVTV QVDNSLGSDSAVLYLHVTCPLE 890
mCS1c     LI QVDFGDGIIVSY VNLSSMEDGIKH VYQNVGIFRVTV QVDNSLGSDSAVLYLHVTCPLE 890
hCS1      LI QVDFGDGIIVSY VNLSSMEDGIKH VYQNVGIFRVTV QVDNSLGSDSAVLYLHVTCPLE 891

mSorLA    NW SDSKSITTIKGV VIQAPNIHIDSY DENSLSFTLTMD GDIKVNQYVNVLFWSFDAHKQE 1610
mSort     -----VLIVKKYVCGGR- 784
Vps10p    SE TDSISYSTDFGK TWKDYKFCADKVLVDITTVPRDS ALRFLLFGEAAD IGGSSFRITYT 1235
mCS2      AL YLEVVPVIGVNQ EVNLTAVLLPLN PNLTVFYVWIGHSLQPLLSLDNSV TTKFTDAGDV 934
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FIG 2F

title: TYPE 2 DIABETES SUSCEPTIBILITY GENES
Inventor(s): Attie/Stoehr/Schueler/Clee
Application No.:
Docket Number: 960296.99080

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                                . . . . . ^ trans-

mSorLA      II TENDHVLLFWKS LALKEKQFNETR GYEIHMSDSAVN LTAYLGNTTDFKVSNLKMGH 1910
mSort      -----
Vps10p      IFFAANFVYDRGIRRNNGGFARFGEIR LGDDGLIENNNT DRVNNIVKSGF YVFSNIGSLL 1464
mCS2      LFAVGAFILYKFKRRKRPGRTVYAQMHNKEQEMTSPVSHSEDAQSTMQGNHSGVLSINS 1150
hCS3      FV GLAVFLIYKFKRKIPWINIYAQVQHDKEQEMIGSVSQSENAPKITLSD FT-EPEELLD 1194
mCS3      FV GLAVFLIYKFKRKIPWINIYAQVQHDKEQEMIGSVSQSENAPKITLSD FT-EPEELLD 1190
mCS1a      FV GLAVFVIYKFKR ----CVFLLLP -----SYPRPPPPSSF CQ-VQKQ--- 1147
mCS1b      FV GLAVFVIYKFKRR----VALPSP SPSAQPGDSSLR LQRPRPATPPSS PK-RGSAGAQ 1164
mCS1c      FV GLAVFVIYKFKRKIPGINVYAQMONEKEQELINPVSHSES RPSVPHPD LR-RPGQLVD 1168
hCS1      FV GLAVFVIYKFKRR----VALPSP SPSTQPGDSSLR LQRARHATPPST PK-RGSAGAQ 1165
            -membrane^ .S1149->P

mSorLA      NYTFTVQARCLFGSQICGEPVLLYDELSSGADA AVIQ AARSTDVA AVVPILFLILLSL 1970
mSort      -----
Vps10p      QHTKTNI AHVISKI RGRFGNRTGPSYSSLIHQFLDEA DLLLAGHDEDAN --DLSSFMDQ 1522
mCS2      RE MHSYLVG----- 1159
hCS3      KE LDTRVIGGIATIANSESTKEIPNCTSV----- 1223
mCS3      KE LDTRVIGSIATIASSESTKEIPNCTSV----- 1219
mCS1a      -----
mCS1b      FAI----- 1167
mCS1c      EK VESQLLGK----- 1178
hCS1      YAI----- 1168

            : . . . . .

mSorLA      GV GFAILYTKHRR LQSSFSAFANSHYSSRLGSAIFSSG DDLGEDDEDAPMITGFSDDVPM 2030
Vps10p      GSNFEIEEDDVPTL EEEHTSYTDQPTTDDVPDALPEGN EENIDRPDSTAP SNENQ----- 1577
            . . . . . : : : : : : : : : : : : : : :

mSorLA      ( VIA 2033

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FIG 2H

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